

1638

RAW SEQUENCE LISTING DATE: 08/30/2000  
 PATENT APPLICATION: US/09/358,321A TIME: 12:47:06

Input Set : A:\50447 rev sequence 12 nov 1999.txt  
 Output Set: N:\CRF3\08302000\I358321A.raw

**ENTERED**

3 <110> APPLICANT: Sukhapinda, Kitisri  
 4 Hasler, James M  
 5 Petell, James K  
 6 Strickland, James A  
 7 Folkerts, Otto  
 9 <120> TITLE OF INVENTION: ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS  
 11 <130> FILE REFERENCE: 50447  
 13 <140> CURRENT APPLICATION NUMBER: US 09/358,321A  
 14 <141> CURRENT FILING DATE: 1999-07-21  
 16 <150> PRIOR APPLICATION NUMBER: US 60/093,587  
 17 <151> PRIOR FILING DATE: 1998-07-21  
 19 <160> NUMBER OF SEQ ID NOS: 56  
 21 <170> SOFTWARE: PatentIn Ver. 2.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 17  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Description of Artificial Sequence:5' primer  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: unsure  
 33 <222> LOCATION: (12)  
 34 <223> OTHER INFORMATION: n can be a,t,g, or c in this degenerate primer  
 36 <400> SEQUENCE: 1

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 40 <210> SEQ ID NO: 2  
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 43 <213> ORGANISM: Artificial Sequence  
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 48 <220> FEATURE:  
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 60 <212> TYPE: DNA  
 61 <213> ORGANISM: Zea mays  
 63 <220> FEATURE:  
 64 <221> NAME/KEY: CDS  
 65 <222> LOCATION: (1)..(276)  
 67 <400> SEQUENCE: 3  
 68 gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act 48  
 69 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr

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70   1           5           10           15
72 ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att   96
73 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
74           20           25           30
76 ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc   144
77 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
78           35           40           45
80 atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac   192
81 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
82           50           55           60
84 act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc   240
85 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
86   65           70           75           80
88 tgc ggc atc atc gcc tca gat gag aag cga cat gaa   276
89 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
90           85           90
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 92
95 <212> TYPE: PRT
96 <213> ORGANISM: Zea mays
98 <400> SEQUENCE: 4
99 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr
100  1           5           10           15
102 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
103           20           25           30
105 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
106           35           40           45
108 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
109           50           55           60
111 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
112   65           70           75           80
114 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
115           85           90
118 <210> SEQ ID NO: 5
119 <211> LENGTH: 1621
120 <212> TYPE: DNA
121 <213> ORGANISM: Zea mays
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (146)..(1324)
127 <220> FEATURE:
128 <221> NAME/KEY: mat_peptide
129 <222> LOCATION: (239)..(1324)
131 <400> SEQUENCE: 5
132 cgcacgcgcc ctctgccgct tgttcgttcc tcgcgctcgc caccaggcac caccacacac 60
134 atcccaatct cgcgaggcca agcagcaggg tctgcggcgg cggcggcggc cgcgcttcgg 120
136 gctccccctt ccattggcct ccacg atg gcg ctc cgc ctc aac gac gtc gcg 172
137           Met Ala Leu Arg Leu Asn Asp Val Ala
138           -30           -25

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140 ctc tgc ctc tcc ccg ccg ctc gcc gcc cgc cgc cgc cgc agc agc 220
141 Leu Cys Leu Ser Pro Pro Leu Ala Ala Arg Arg Arg Arg Arg Ser Ser
142 -20 -15 -10
144 ggc agg ttc gtc gcc gtc gcc tcc atg acg tcc gcc gtc tcc acc aag 268
145 Gly Arg Phe Val Ala Val Ala Ser Met Thr Ser Ala Val Ser Thr Lys
146 -5 -1 1 5 10
148 gtc gag aat aag aag cca ttt gct cct cca agg gag gta cat gtc cag 316
149 Val Glu Asn Lys Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln
150 15 20 25
152 gtt aca cat tca atg cca cct cac aag att gaa att ttc aag tcg ctt 364
153 Val Thr His Ser Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu
154 30 35 40
156 gat gat tgg gct aga gat aat atc ttg acg cat ctc aag cca gtc gag 412
157 Asp Asp Trp Ala Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu
158 45 50 55
160 aag tgt tgg cag cca cag gat ttc ctc ccg gac cca gca tct gaa gga 460
161 Lys Cys Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly
162 60 65 70
164 ttt cat gat gaa gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct 508
165 Phe His Asp Glu Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro
166 75 80 85 90
168 gat gat tat ttt gtt ttg gtg gga gac atg att acc gag gaa gct 556
169 Asp Asp Tyr Phe Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala
170 95 100 105
172 cta cca aca tac cag act atg ctt aac acc ctc gac ggt gtc aga gat 604
173 Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp
174 110 115 120
176 gag aca ggt gca agc ccc act gcc tgg gct gtt tgg acg agg gca tgg 652
177 Glu Thr Gly Ala Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp
178 125 130 135
180 act gct gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac 700
181 Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr
182 140 145 150
184 ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat 748
185 Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr
186 155 160 165 170
188 ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt 796
189 Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu
190 175 180 185
192 ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac 844
193 Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
194 190 195 200
196 ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca 892
197 Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala
198 205 210 215
200 caa atc tgc gcc atc atc gcc tca gat gag aag cga cat gaa act gcg 940
201 Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala
202 220 225 230
204 tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc 988

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205 Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr
206 235      240      245      250
208 gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc 1036
209 Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala
210      255      260      265
212 cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc 1084
213 His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser
214      270      275      280
216 atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac 1132
217 Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp
218      285      290      295
220 atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt 1180
221 Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly
222      300      305      310
224 ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct 1228
225 Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala
226 315      320      325      330
228 tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa 1276
229 Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys
230      335      340      345
232 gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg 1324
233 Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
234      350      355      360
236 tgagatcgga aacctgtgc ggactgctta gacaagacct gctgtgtctg cgttacatag 1384
238 gtctccaggt ttgatcaaa tggccccgtg tcgtcttata gagcgatagg agaacgtgtt 1444
240 ggtctgtggt gtagctttgt ttttattttg tatttttctg ctttgatgta caacctgtgg 1504
242 ccgcataaac tggggcgtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg 1564
244 gtgtgtttcg gtatgttatt tgagttgctc agatctgtta aaaaaaaaaa aaaaaaa 1621
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248 <211> LENGTH: 393
249 <212> TYPE: PRT
250 <213> ORGANISM: Zea mays
252 <400> SEQUENCE: 6
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254 -30      -25      -20
256 Ala Ala Arg Arg Arg Arg Arg Ser Ser Gly Arg Phe Val Ala Val Ala
257 -15      -10      -5      -1 1
259 Ser Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys Pro Phe
260      5      10      15
262 Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro
263      20      25      30
265 His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asp Asn
266      35      40      45
268 Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp
269 50      55      60      65
271 Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val Lys Glu
272      70      75      80
274 Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Cys Leu
275      85      90      95

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```

277 Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
278      100      105      110
280 Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr
281      115      120      125
283 Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
284 130      135      140      145
286 Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Met
287      150      155      160
289 Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp
290      165      170      175
292 Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe
293      180      185      190
295 Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg His Ala
296      195      200      205
298 Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile Ile Ala
299 210      215      220      225
301 Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys
302      230      235      240
304 Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala Asp Met
305      245      250      255
307 Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
308      260      265      270
310 Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
311      275      280      285
313 Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
314 290      295      300      305
316 Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
317      310      315      320
319 Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
320      325      330      335
322 Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
323      340      345      350
325 Trp Val Tyr Gly Arg Asp Val Gln Leu
326      355      360
329 <210> SEQ ID NO: 7
330 <211> LENGTH: 30
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
337 <400> SEQUENCE: 7
338 atggctagcc tccgcctcaa cgacgtcgcg 30
341 <210> SEQ ID NO: 8
342 <211> LENGTH: 36
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
349 <400> SEQUENCE: 8

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 08/30/2000

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TIME: 12:47:07

Input Set : A:\50447 rev sequence 12 nov 1999.txt

Output Set: N:\CRF3\08302000\I358321A.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21